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<!--StartFragment-->RESULT 5
ABX62889
ID    ABX62889 standard; cDNA; 3622 BP.
XX
AC    ABX62889;
XX
DT    25-FEB-2003 (first entry)
XX
DE    Human activated T cell cDNA #5.
XX
KW    T cell; gene; ss; differential expression; T cell activation;
KW    antiallergic; cytostatic; immunosuppressive; antimicrobial; gene therapy;
KW    allergy; cancer; graft versus host disease; infection;
KW    autoimmune disorder.
XX
OS    Homo sapiens.
XX
PN    US2002137077-A1.
XX
PD    26-SEP-2002.
XX
PF    25-OCT-2001; 2001US-00002600.
XX
PR    25-OCT-2000; 2000US-0243521P.
XX
PA    (HOPK/) HOPKINS C M.
PA    (PETE/) PETERSON D P.
PA    (COCK/) COCKS B G.
PA    (HAWK/) HAWKINS P R.
XX
PI    Hopkins CM, Peterson DP, Cocks BG, Hawkins PR;
XX
DR    WPI; 2003-102381/09.
XX
PT    New combination comprising several cDNAs that are differentially
PT    expressed in activated T cells, useful for diagnosing, treating, staging
PT    or monitoring treatment for allergy, cancer, infectious and/or autoimmune
PT    disorders.
XX
PS    Claim 1; Page; 180pp; English.
XX
CC    This invention relates to the sequences of several cDNAs that are
CC    differentially expressed in activated T cells. The sequences of the
CC    invention may have antiallergic, cytostatic, immunosuppressive and
CC    antimicrobial activity and may be used in gene therapy. The invention
CC    also comprises a method for screening samples for differentially
CC    expressed genes and a method for detecting these cDNAs by hybridisation.
CC    The methods and compositions of the present invention are useful for
CC    diagnosing, treating, staging or monitoring treatment for allergy,
CC    cancer, chronic graft versus host disease, infectious and/or autoimmune
CC    disorders. The present sequence represents a cDNA of the invention that
CC    is differentially expressed in activated T cells
XX
SQ    Sequence 3622 BP; 965 A; 838 C; 902 G; 916 T; 0 U; 1 Other;

Query Match          92.6%; Score 3125.6; DB 8; Length 3622;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3292; Conservative 0; Mismatches 35; Indels 96; Gaps 5;

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Qy          12 CTCCGCCCGCCCGGTGCGGGTGCTCCGCTACCGGCTCCTCTCCGTTCTGTGCTCTCTT 71
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Db	1	CTCTGCGGGCCGCGGGTGCGGGTGCTCCGCTACCGGCT-CTCTCCGTTCTGTGCTCTCTT	59
Qy	72	CTGCTCTCGGCTCCCCACCCCCTCTCCCTTCCCTCCTCTCCCCCTTGCTCCCCCTCCTCTG	131
Db	60	CTGCTCTCGGCTCCCCACCCCCTCTCCCTTCCCTCCTCTCCCCCTTGCNTCCCCCTCCTCTG	119
Qy	132	CAGCGCCTGCATTATTTTCTGCCCCGAGGCTCGGCTTGCACTGCTGCTGCAGCCCGGGGA	191
Db	120	CAGCGCCTGCATTATTTTCTGCCCCGAGGCTCGGCTTGCACTGCTGCTGCAGCCCGGGGA	179
Qy	192	GGTGGCTGGGTGGGTGGGGAGGAGACTGTGCAAGTTGTAGGGGAGGGGGTGCCCTCTTCT	251
Db	180	GGTGGCTGGGTGGGTGGGGAGGAGACTGTGCAAG-TGTAGGGGAGGGGGTGCCCTCTTCT	238
Qy	252	TCCCCGCTCCCTTCCCCCGCCAACTCCTTCCCTCCTTCTCCCCCTTTCCCTCCCCGCC	311
Db	239	TCCCCGCTCCCTTCCCCAGCCAAGTGGTTCCCTCCTTCTCCCCCTTTCCCTCCCAGCC	298
Qy	312	CCCACCTTCTTCTCCTTTTCGGAAGGACTGGTAACTTGTGCTGCGGAGCGAACGGCGGCG	371
Db	299	CCCACCTTCTTCTCCTTTTCGGAAGGGCTGGTAACTTGTGCTGCGGAGCGAA-----	350
Qy	372	GCGGCGGCGGCGGCGGCACCATCCAGGCGGGCACCATGGGCACGTCCGCGCTCTGGGCGC	431
Db	351	-CGGCGGCGGCGGCGGCACCATCCAGGCGGGCACCATGGGCACGTCCGCGCTCTGGGCGC	409
Qy	432	TCTGGCTGCTGCTCGCGCTGTGCTGGGCGCCCCGGGAGAGCGGCGCCACCGGAACCGGGA	491
Db	410	TCTGGCTGCTGCTCGCGCTGTGCTGGGCGCCCCGGGAGAGCGGCGCCACCGGAACCGGGA	469
Qy	492	GAAAAGCCAAATGTGAACCTCCCAATTCCAGTGCACAAATGGTCGCTGTATTACGCTGT	551
Db	470	GAAAAGCCAAATGTGAACCTCCCAATTCCAGTGCACAAATGGTCGCTGTATTACGCTGT	529
Qy	552	TGTGGAAATGTGATGGGGATGAAGACTGTGTTGACGGCAGTGATGAAAAGAACTGTGTAA	611
Db	530	TGTGGAAATGTGATGGGGATGAAGACTGTGTTGACGGCAGTGATGAAAAGAACTGTGTAA	589
Qy	612	AGAAGACGTGTGCTGAATCTGACTTCGTGTGCAACAATGGCCAGTGTGTTCCAGCCGAT	671
Db	590	AGAAGACGTGTGCTGAATCTGACTTCGTGTGCAACAATGGCCAGTGTGTTCCAGCCGAT	649
Qy	672	GGAAGTGTGATGGAGATCCTGACTGCGAAGATGGTTCAGATGAAAGCCCAGAACAGTGCC	731
Db	650	GGAAGTGTGATGGAGATCCTGACTGCGAAGATGGTTCAGATGAAAGCCCAGAACAGTGCC	709
Qy	732	ATATGAGAACATGCCGCATACATGAAATCAGCTGTGGCGCCCATTCTACTCAGTGTATCC	791
Db	710	ATATGAGAACATGCCGCATACATGAAATCAGCTGTGGCGCCCATTCTACTCAGTGTATCC	769
Qy	792	CAGTGTCTTGAGATGTGATGGTGAAAATGATTGTGACAGTGGAGAAGATGAAGAAAAC	851
Db	770	CAGTGTCTTGAGATGTGATGGTGAAAATGATTGTGACAGTGGAGAAGATGAAGAAAAC	829
Qy	852	GTGGCAATATAACATGTAGTCCCACGAGTTCACCTGCTCCAGTGGCCGCTGCATCTCCA	911
Db	830	GTGGCAATATAACATGTAGTCCCACGAGTTCACCTGCTCCAGTGGCCGCTGCATCTCCA	889
Qy	912	GGAACCTTTGTATGCAATGGCCAGGATGACTGCAGCGATGGCAGTGATGAGCTGGACTGTG	971
Db	890	GGAACCTTTGTATGCAATGGCCAGGATGACTGCAGCGATGGCAGTGATGAGCTGGACTGTG	949

Qy	972	CCCCGCCAACCTGTGGCGCCCATGAGTTCCAGTGCAGCACCTCCTCCTGCATCCCCATCA	1031
Db	950	CCCCGCCAACCTGTGGCGCCCATGAGTTCCAGTGCAGCACCTCCTCCTGCATCCCCATCA	1009
Qy	1032	GCTGGGTATGCGACGATGATGCAGACTGCTCCGACCAATCTGATGAGTCCCTGGAGCAGT	1091
Db	1010	GCTGGGTATGCGACGATGATGCAGACTGCTCCGACCAATCTGATGAGTCCCTGGAGCAGT	1069
Qy	1092	GTGGCCGTCAGCCAGTCATACACACCAAGTGTCCAGCCAGCGAAATCCAGTGC GGCTCTG	1151
Db	1070	GTGGCCGTCAGCCAGTCATACACACCAAGTGTCCAGCCAGCGAAATCCAGTGC GGCTCTG	1129
Qy	1152	GCGAGTGCATCCATAAGAAGTGGCGATGTGATGGGGACCCTGACTGCAAGGATGGCAGTG	1211
Db	1130	GCGAGTGCATCCATAAGAAGTGGCGATGTGATGGGGACCCTGACTGCAAGGATGGCAGTG	1189
Qy	1212	ATGAGGTCAACTGTCCCTCTCGAACTTGCCGACCTGACCAATTTGAATGTGAGGATGGCA	1271
Db	1190	ATGAGGTCAACTGTCCCTCTCGAACTTGCCGACCTGACCAATTTGAATGTGAGGATGGCA	1249
Qy	1272	GCTGCATCCATGGCAGCAGGCAGTGAATGGTATCCGAGACTGTGTCGATGGTTCCGATG	1331
Db	1250	GCTGCATCCATGGCAGCAGGCAGTGAATGGTATCCGAGACTGTGTCGATGGTTCCGATG	1309
Qy	1332	AAGTCAACTGCAAAAATGTCAATCAGTGCTTGGGCCCTGGAAAATTCAAGTGCAGAAAGTG	1391
Db	1310	AAGTCAACTGCAAAAATGTCAATCAGTGCTTGGGCCCTGGAAAATTCAAGTGCAGAAAGTG	1369
Qy	1392	GAGAATGCATAGATATCAGCAAAGTATGTAACCAGGAGCAGGACTGCAGGGACTGGAGTG	1451
Db	1370	GAGAATGCATAGATATCAGCAAAGTATGTAACCAGGAGCAGGACTGCAGGGACTGGAGTG	1429
Qy	1452	ATGAGCCCCTGAAAGAGTGT CATATAAACGAATGCTTGGTAAATAATGGTGGATGTTCTC	1511
Db	1430	ATGAGCCCCTGAAAGAGTGT CATATAAACGAATGCTTGGTAAATAATGGTGGATGTTCTC	1489
Qy	1512	ATATCTGCAAAGACCTAGTTATAGGCTACGAGTGTGACTGTGCAGCTGGGTTTGAAGTGA	1571
Db	1490	ATATCTGCAAAGACCTAGTTATAGGCTACGAGTGTGACTGTGCAGCTGGGTTTGAAGTGA	1549
Qy	1572	TAGATAGGAAAACCTGTGGAGATATTGATGAATGCCAAAATCCAGGAATCTGCAGTCAAA	1631
Db	1550	TAGATAGGAAAACCTGTGGAGATATTGATGAATGCCAAAATCCAGGAATCTGCAGTCAAA	1609
Qy	1632	TTTGTATCAACTTAAAAGGCGGTTACAAGTGTGAATGTAGTCGTGGCTATCAAATGGATC	1691
Db	1610	TTTGTATCAACTTAAAAGGCGGTTACAAGTGTGAATGTAGTCGTGGCTATCAAATGGATC	1669
Qy	1692	TTGCTACTGGCGTGTGCAAGGCAGTAGGCAAAGAGCCAAGTCTGATCTTCACTAATCGAA	1751
Db	1670	TTGCTACTGGCGTGTGCAAGGCAGTAGGCAAAGAGCCAAGTCTGATCTTCACTAATCGAA	1729
Qy	1752	GAGACATCAGGAAGATTGGCTTAGAGAGGAAAGAATATATCCAACCTAGTTGAACAGCTAA	1811
Db	1730	GAGACATCAGGAAGATTGGCTTAGAGAGGAAAGAATATATCCAACCTAGTTGAACAGCTAA	1789
Qy	1812	GAAACACTGTGGCTCTCGATGCTGACATTGCTGCCCAGAACTATTCTGGGCCGATCTAA	1871
Db	1790	GAAACACTGTGGCTCTCGATGCTGACATTGCTGCCCAGAACTATTCTGGGCCGATCTAA	1849

Qy	1872	GCCAAAAGGCTATCTTCAGTGCCTCAATTGATGACAAGGTTGGTAGACATGTTAAAATGA	1931
Db	1850	GCC-AAAGGCTATCTTCAGTGCCTCAATTGATGACAAGGTTGGTAGACATGTTAAAATGA	1908
Qy	1932	TCGACAATGTCTATAATCCTGCAGCCATTGCTGTTGATTGGGTGTACAAGACCATCTACT	1991
Db	1909	TCGACAATGTCTATAATCCTGCAGCCATTGCTGTTGATTGGGTGTACAAGACCATCTACT	1968
Qy	1992	GGACTGATGCGGCTTCTAAGACTATTTTCAGTAGCTACCCTAGATGGAACCAAGAGGAAGT	2051
Db	1969	GGACTGATGCGGCTTCTAAGACTATTTTCAGTAGCTACCCTAGATGGAACCAAGAGGAAGT	2028
Qy	2052	TCCTGTTTAACTCTGACTTGCGAGAGCCTGCCTCCATAGCTGTGGACCCACTGTCTGGCT	2111
Db	2029	TCCTGTTTAACTCTGACTTGCGAGAGCCTGCCTCCATAGCTGTGGACCCACTGTCTGGCT	2088
Qy	2112	TTGTTTACTGGTCAGACTGGGGTGAACCAGCTAAAATAGAAAAAGCAGGAATGAATGGAT	2171
Db	2089	TTGTTTACTGGTCAGACTGGGGTGAACCAGCTAAAATAGAAAAAGCAGGAATGAATGGAT	2148
Qy	2172	TCGATAGACGTCCACTGGTGACAGCGGATATCCAGTGGCCTAACGGAATTACACTTGACC	2231
Db	2149	TCGATAGACGTCCACTGGTGACAGCGGATATCCAGTGGCCTAACGGAATTACACTTGACC	2208
Qy	2232	TTATAAAAAGTCGCCTCTATTGGCTTGATTCTAAGTTGCACATGTTATCCAGCGTGGACT	2291
Db	2209	TTATAAAAAGTCGCCTCTATTGGCTTGATTCTAAGTTGCACATGTTATCCAGCGTGGACT	2268
Qy	2292	TGAATGGCCAAGATCGTAGGATAGTACTAAAGTCTCTGGAGTTCCTAGCTCATCCTCTTG	2351
Db	2269	TGAATGGCCAAGATCGTAGGATAGTACTAAAGTCTCTGGAGTTCCTAGCTCATCCTCTTG	2328
Qy	2352	CACTAACAATATTTGAGGATCGTGTCTACTGGATAGATGGGGAAAATGAAGCAGTCTATG	2411
Db	2329	CACTAACAATATTTGAGGATCGTGTCTACTGGATAGATGGGGAAAATGAAGCAGTCTATG	2388
Qy	2412	GTGCCAATAAATTCACTGGATCAGAGCTAGCCACTCTAGTCAACAACCTGAATGATGCCC	2471
Db	2389	GTGCCAATAAATTCACTGGATCAGAGCTAGCCACTCTAGTCAACAACCTGAATGATGCCC	2448
Qy	2472	AAGACATCATTGTCTATCATGAACTTGACAGCCATCAGGTAAAAATTGGTGTGAAGAAG	2531
Db	2449	AAGACATCATTGTCTATCATGAACTTGACAGCCATCAGGTAAAAATTGGTGTGAAGAAG	2508
Qy	2532	ACATGGAGAATGGAGGATGTGAATACCTATGCCTGCCAGCACCACAGATTAATGATCACT	2591
Db	2509	ACATGGAGAATGGAGGATGTGAATACCTATGCCTGCCAGCACCACAGATTAATGATCACT	2568
Qy	2592	CTCCAAAATATACCTGTTTCCTGTCCAGTGGGTACAATGTAGAGGAAAATGGCCGAGACT	2651
Db	2569	CTCCAAAATATACCTGTTTCCTGTCCAGTGGGTACAATGTAGAGGAAAATGGCCGAGACT	2628
Qy	2652	GTCAAA-----	2657
Db	2629	GTCAAAGTACTGCAACTACTGTGACTTACAGTGAGACAAAAGATACGAACACAACAGAAA	2688
Qy	2658	-----GGATCAATGTGACCACAGCAGTATCAGAGG	2687
Db	2689	TTTCAGCAACTAGTGGACTAGTTCCTGGAGGGATCAATGTGACCACAGCAGTATCAGAGG	2748
Qy	2688	TCAGTGTTCCCCCAAAGGGACTTCTGCCGCATGGGCCATTCTTCCTCTCTTGCTCTTAG	2747

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Db      2749 TCAGTGTTCCCCCAAAGGGACTTCTGCCGCATGGGCCATTCTTCCTCTCTTGCTCTTAG 2808
Qy      2748 TGATGGCAGCAGTAGGTGGCTACTTGATGTGGCGGAATTGGCAACACAAGAACATGAAAA 2807
      |||
Db      2809 TGATGGCAGCAGTAGGTGGCTACTTGATGTGGCGGAATTGGCAACACAAGAACATGAAAA 2868
Qy      2808 GCATGAACTTTGACAATCCTGTGTACTTGAAAACCACTGAAGAGGACCTCTCCATAGACA 2867
      |||
Db      2869 GCATGAACTTTGACAATCCTGTGTACTTGAAAACCACTGAAGAGGACCTCTCCATAGACA 2928
Qy      2868 TTGGTAGACACAGTGCTTCTGTTGGACACACGTACCCAGCAATATCAGTTGTAAGCACAG 2927
      |||
Db      2929 TTGGTAGACACAGTGCTTCTGTTGGACACACGTACCCAGCAATATCAGTTGTAAGCACAG 2988
Qy      2928 ATGATGATCTAGCTTGACTTCTGTGACAAATGTTGACCTTTGAGGTCTAAACAAATAATA 2987
      |||
Db      2989 ATGATGATCTAGCTTGACTTCTGTGACAAATGTTGACCTTTGAGGTCTAAACAAATAATA 3048
Qy      2988 CCCCCGTCGGAATGGTAACCGAGCCAGCAGCTGAAGTCTCTTTTTCTTCCTCTCGGCTGG 3047
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Db      3049 CCCCCGTCGGAATGGTAACCGAGCCAGCAGCTGAAGTCTCTTTTTCTTCCTCTCGGCTGG 3108
Qy      3048 AAGAACATCAAGATACCTTTGCGTGGATCAAGCTTGTGTACTTGACCGTTTTTATATTAC 3107
      |||
Db      3109 AAGAACATCAAGATACCTTTGCGTGGATCAAGCTTGTGTACTTGACCGTTTTTATATTAC 3168
Qy      3108 TTTTGTAATATTCTTGTCCACATTCTACTTCAGCTTTGGATGTGGTTACCGAGTATCTG 3167
      |||
Db      3169 TTTTGTAATATTCTTGTCCACATTCTACTTCAGCTTTGGATGTGGTTACCGAGTATCTG 3228
Qy      3168 TAACCCTTGAATTTCTAGACAGTATTGCCACCTCTGGCCAAATATGCACTTTCCCTAGAA 3227
      |||
Db      3229 TAACCCTTGAATTTCTAGACAGTATTGCCACCTCTGGCCAAATATGCACTTTCCCTAGAA 3288
Qy      3228 AGCCATATTCCAGCAGTGAAACTTGTGCTATAGTGTATACCACCTGTACATACATTGTAT 3287
      |||
Db      3289 AGCCATATTCCAGCAGTGAAACTTGTGCTATAGTGTATACCACCTGTACATACATTGTAT 3348
Qy      3288 AGGCCATCTGTAAATATCCCGACAAAACGGGTTACTAAGATGAAATTGCCAAAAAAATT 3347
      |||
Db      3349 AGGCCATCTGTAAATATCCAGAGAACAATCACTATTCTTAAGCACTTTGAAAATATTTC 3408
Qy      3348 TAT 3350
      |||
Db      3409 TAT 3411
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<!--EndFragment-->